

OIPE

#2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/836,602

DATE: 05/22/2001

TIME: 11:20:49

Input Set : A:\seqlist.txt

Output Set: C:\CRF3\05222001\I836602.raw

ENTERED

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7 <110> APPLICANT: Prof. Dr. Axel R. Zander
9 <120> TITLE OF INVENTION: Use of CD34 or a Polypeptide derived therefrom as
10 Cell Surface/Gene Transfer Marker
12 <130> FILE REFERENCE: 35-204
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/836,602
C--> 15 <141> CURRENT FILING DATE: 2001-05-22
17 <160> NUMBER OF SEQ ID NOS: 10
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1122
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1122)
29 <223> OTHER INFORMATION: CD34 (complete length)
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34 1 5 10 15
36 ggg ttc atg agt ctt gac aac aac ggt act gct acc cca gag tta cct 96
37 Gly Phe Met Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro
38 20 25 30
40 acc cag gga aca ttt tca aat gtt tct aca aat gta tcc tac caa gaa 144
41 Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu
42 35 40 45
44 act aca aca cct agt acc ctt gga agt acc agc ctg cac cct gtg tct 192
45 Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
46 50 55 60
48 caa cat ggc aat gag gcc aca aca aac atc aca gaa acg aca gtc aaa 240
49 Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
50 65 70 75 80
52 ttc aca tct acc tct gtg ata acc tca gtt tat gga aac aca aac tct 288
53 Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
54 85 90 95
56 tct gtc cag tca cag acc tct gta atc agc aca gtg ttc acc acc cca 336
57 Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
58 100 105 110
60 gcc aac gtt tca act cca gag aca acc ttg aag cct agc ctg tca cct 384
61 Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
62 115 120 125
64 gga aat gtt tca gac ctt tca acc act agc act agc ctt gca aca tct 432
65 Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser
66 130 135 140
68 ccc act aaa ccc tat aca tca tct tct cct atc cta agt gac atc aag 480
69 Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
70 145 150 155 160

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72 gca gaa atc aaa tgt tca ggc atc aga gaa gtg aaa ttg act cag ggc 528
73 Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
74 165 170 175
76 atc tgc ctg gag caa aat aag acc tcc agc tgt gcg gag ttt aag aag 576
77 Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
78 180 185 190
80 gac agg gga gag ggc ctg gcc cga gtg ctg tgt ggg gag gag cag gct 624
81 Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
82 195 200 205
84 gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct 672
85 Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser
86 210 215 220
88 gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa 720
89 Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu
90 225 230 235 240
92 att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa 768
93 Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys
94 245 250 255
96 aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag 816
97 Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln
98 260 265 270
100 agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg 864
101 Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu
102 275 280 285
104 ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat cgc cgc agc 912
105 Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser
106 290 295 300
108 tgg agc ccc aca gga gaa agg ctg ggc gaa gac cct tat tac acg gaa 960
109 Trp Ser Pro Thr Gly Glu Arg Leu Gly Glu Asp Pro Tyr Tyr Thr Glu
110 305 310 315 320
112 aac ggt gga ggc cag ggc tat agc tca gga cct ggg acc tcc cct gag 1008
113 Asn Gly Gly Gly Gln Gly Tyr Ser Ser Gly Pro Gly Thr Ser Pro Glu
114 325 330 335
116 gct cag gga aag gcc agt gtg aac cga ggg gct cag gaa aac ggg acc 1056
117 Ala Gln Gly Lys Ala Ser Val Asn Arg Gly Ala Gln Glu Asn Gly Thr
118 340 345 350
120 ggc cag gcc acc tcc aga aac ggc cat tca gca aga caa cac gtg gtg 1104
121 Gly Gln Ala Thr Ser Arg Asn Gly His Ser Ala Arg Gln His Val Val
122 355 360 365
124 gct gat acc gaa ttg tga 1122
125 Ala Asp Thr Glu Leu
126 370
130 <210> SEQ ID NO: 2
131 <211> LENGTH: 373
132 <212> TYPE: PRT
133 <213> ORGANISM: Homo sapiens
135 <400> SEQUENCE: 2
136 Met Pro Arg Gly Trp Thr Ala Leu Cys Leu Leu Ser Leu Leu Pro Ser
137 1 5 10 15

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138 Gly Phe Met Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro
139          20          25          30
140 Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu
141          35          40          45
142 Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
143          50          55          60
144 Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
145          65          70          75          80
146 Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
147          85          90          95
148 Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
149          100          105          110
150 Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
151          115          120          125
152 Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser
153          130          135          140
154 Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
155          145          150          155          160
156 Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
157          165          170          175
158 Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
159          180          185          190
160 Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
161          195          200          205
162 Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser
163          210          215          220
164 Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu
165          225          230          235          240
166 Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys
167          245          250          255
168 Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln
169          260          265          270
170 Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu
171          275          280          285
172 Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser
173          290          295          300
174 Trp Ser Pro Thr Gly Glu Arg Leu Gly Glu Asp Pro Tyr Tyr Thr Glu
175          305          310          315          320
176 Asn Gly Gly Gly Gln Gly Tyr Ser Ser Gly Pro Gly Thr Ser Pro Glu
177          325          330          335
178 Ala Gln Gly Lys Ala Ser Val Asn Arg Gly Ala Gln Glu Asn Gly Thr
179          340          345          350
180 Gly Gln Ala Thr Ser Arg Asn Gly His Ser Ala Arg Gln His Val Val
181          355          360          365
182 Ala Asp Thr Glu Leu
183          370
190 <210> SEQ ID NO: 3
191 <211> LENGTH: 951
192 <212> TYPE: DNA

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193 <213> ORGANISM: Homo sapiens
195 <220> FEATURE:
196 <221> NAME/KEY: CDS
197 <222> LOCATION: (1)..(951)
198 <223> OTHER INFORMATION: CD34 (truncated variant)
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203   1           5           10           15
205 ggg ttc atg agt ctt gac aac aac ggt act gct acc cca gag tta cct      96
206 Gly Phe Met Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro
207           20           25           30
209 acc cag gga aca ttt tca aat gtt tct aca aat gta tcc tac caa gaa     144
210 Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu
211           35           40           45
213 act aca aca cct agt acc ctt gga agt acc agc ctg cac cct gtg tct     192
214 Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
215           50           55           60
217 caa cat ggc aat gag gcc aca aca aac atc aca gaa acg aca gtc aaa     240
218 Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
219   65           70           75           80
221 ttc aca tct acc tct gtg ata acc tca gtt tat gga aac aca aac tct     288
222 Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
223           85           90           95
225 tct gtc cag tca cag acc tct gta atc agc aca gtg ttc acc acc cca     336
226 Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
227           100          105          110
229 gcc aac gtt tca act cca gag aca acc ttg aag cct agc ctg tca cct     384
230 Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
231           115          120          125
233 gga aat gtt tca gac ctt tca acc act agc act agc ctt gca aca tct     432
234 Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser
235           130          135          140
237 ccc act aaa ccc tat aca tca tct tct cct atc cta agt gac atc aag     480
238 Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
239 145           150          155          160
241 gca gaa atc aaa tgt tca ggc atc aga gaa gtg aaa ttg act cag ggc     528
242 Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
243           165          170          175
245 atc tgc ctg gag caa aat aag acc tcc agc tgt gcg gag ttt aag aag     576
246 Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
247           180          185          190
249 gac agg gga gag ggc ctg gcc cga gtg ctg tgt ggg gag gag cag gct     624
250 Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
251           195          200          205
253 gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct     672
254 Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser
255           210          215          220
257 gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa     720

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258 Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu
259 225                230                235                240
261 att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa    768
262 Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys
263                245                250                255
265 aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag    816
266 Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln
267                260                265                270
269 agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg    864
270 Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu
271                275                280                285
273 ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat cgc cgc agc    912
274 Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser
275                290                295                300
277 tgg agc ccc aca gga gaa agg ctg gaa cta gaa cca tga    951
278 Trp Ser Pro Thr Gly Glu Arg Leu Glu Leu Glu Pro
279 305                310                315
285 <210> SEQ ID NO: 4
286 <211> LENGTH: 316
287 <212> TYPE: PRT
288 <213> ORGANISM: Homo sapiens
290 <400> SEQUENCE: 4
291 Met Pro Arg Gly Trp Thr Ala Leu Cys Leu Leu Ser Leu Leu Pro Ser
292 1          5          10          15
293 Gly Phe Met Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro
294                20          25          30
295 Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu
296                35          40          45
297 Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
298                50          55          60
299 Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
300 65          70          75          80
301 Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
302                85          90          95
303 Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
304                100         105         110
305 Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
306                115         120         125
307 Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser
308                130         135         140
309 Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
310 145         150         155         160
311 Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
312                165         170         175
313 Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
314                180         185         190
315 Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
316                195         200         205
317 Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser

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VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

Output Set: C:\CRF3\05222001\I836602.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date